



SEQUENCE LISTING

<110> Fujisawa Pharmaceutical Co., Ltd.
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Aramori, Ichiro

<120> New methods for selecting an immunosuppressive agent

<130> 274130US0PCT
<140> 10/540,546
<141> 2005-06-24

<150> JP2002-378800
<151> 2002-12-27

<160> 86

<170> PatentIn version 3.1

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<213> Homo sapiens

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<223> human histone deacetylase-4 (HDAC4) gene

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Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro		
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Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln		
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Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln		
85 90 95		
cac gag cag ctc tcc cgg cag cac gag gcg cag ctc cac gag cac atc		336
His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile		
100 105 110		
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Gly	His	His	Ala	Glu	Glu	Ser	Thr	Pro	Met	Gly	Phe	Cys	Tyr	Phe	Asn	
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tcc	gtg	gcc	gtg	gca	gcc	aag	ctt	ctg	cag	cag	agg	ttg	agc	gtg	agc	2496
Ser	Val	Ala	Ala	Ala	Lys	Leu	Leu	Gln	Gln	Arg	Leu	Ser	Val	Ser		
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aag	atc	ctc	atc	gtg	gac	tgg	gac	gtg	cac	cat	gga	aac	ggg	acc	cag	2544
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acc gcc atg gcc tcg ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg 1060 1065 1070	3216
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Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
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Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
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Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
85 90 95
His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
100 105 110
Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu
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Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu
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Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys
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Glu Phe Val Leu Asn Lys Lys Ala Leu Ala His Arg Asn Leu Asn
180 185 190
His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His
195 200 205
Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser
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Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro
225 230 235 240
Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu
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Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys
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Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr
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Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg		
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Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro		
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Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala		
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Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg		
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Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser		
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Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu		
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Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr		
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Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His		
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 Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu
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 Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser
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 Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg
 675 680 685
 Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg
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 770 775 780
 Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro
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 Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn
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 820 825 830
 Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln
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 Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg
 850 855 860
 Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val
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Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His
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Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg
 995 1000 1005

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 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
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 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
 35 40 45

atg gac ctg cgc ctg gac cac cag ttc tca ctg cct gtg gca gag ccg 192
 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
 50 55 60

gcc ctg cgg gag cag cag ctg cag cag gag ctc ctg gcg ctc aag cag 240
 Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
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Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
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cac gag cag ctc tcc cgg cag cac gag gcg cag ctc cac gag cac atc
 His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
 100 105 110

aag caa caa cag gag atg ctg gcc atg aag cac cag cag gag ctg ctg
 Lys Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu
 115 120 125

gaa cac cag cgg aag ctg gag agg cac cgc cag gag cag gag ctg gag
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 130 135 140

aag cag cac cgg gag cag aag ctg cag cag ctc aag aac aag gag aag
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 145 150 155 160

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 Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln
 165 170 175

gaa ttt gtc ctc aat aaa aag aag gcg ctg gcc cac cgg aat ctg aac
 Glu Phe Val Leu Asn Lys Lys Ala Leu Ala His Arg Asn Leu Asn
 180 185 190

cac tgc att tcc agc gac cct cgc tac tgg tac ggg aaa acg cag cac
 His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His
 195 200 205

agt tcc ctt gac cag agt tct cca ccc cag agc gga gtg tcg acc tcc
 Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser
 210 215 220

tat aac cac ccc gtc ctg gga atg tac gac gcc aaa gat gac ttc cct
 Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro
 225 230 235 240

ctt agg aaa aca gct tct gaa ccg aat ctg aaa tta cgg tcc agg cta
 Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu
 245 250 255

aag cag aaa gtg gcc gaa aga cgg agc agc ccc ctg tta cgc agg aaa
 Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys
 260 265 270

gac ggg cca gtg gtc act gct cta aaa aag cgt ccg ttg gat gtc aca
 Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr
 275 280 285

gac tcc gcg tgc agc agc gcc cca ggc tcc gga ccc agc tca ccc aac
 Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn
 290 295 300

aac agc tcc ggg agc gtc agc gcg gag aac ggt atc gcg ccc gcc gtc
 Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val
 305 310 315 320

ccc agc atc ccc gcg gag acg agt ttg gcg cac aga ctt gtg gca cga
 Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg
 330 335 340 345

325	330	335	
gaa ggc tcg gcc gct cca ctt ccc ctc tac aca tcg cca tcc ttg ccc Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro 340	345	350	1056
aac atc acg ctg ggc ctg cct gcc acc ggc ccc tct gcg ggc acg gcg Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala 355	360	365	1104
ggc cag cag gac acc gag aga ctc acc ctt ccc gcc ctc cag cag agg Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg 370	375	380	1152
ctc tcc ctt ttc ccc ggc acc cac ctc act ccc tac ctg agc acc tcg Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser 385	390	395	1200
ccc ttg gag cgg gac gga ggg gca gcg cac agc cct ctt ctg cag cac Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His 405	410	415	1248
atg gtc tta ctg gag cag cca ccg gca caa gca ccc ctc gtc aca ggc Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly 420	425	430	1296
ctg gga gca ctg ccc ctc cac gca cag tcc ttg gtt ggt gca gac cgg Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg 435	440	445	1344
gtg tcc ccc tcc atc cac aag ctg cgg cag cac cgc cca ctg ggg cgg Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg 450	455	460	1392
acc cag tcg gcc ccg ctg ccc cag aac gcc cag gct ctg cag cac ctg Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu 465	470	475	1440
gtc atc cag cag cat cag cag ttt ctg gag aaa cac aag cag cag Val Ile Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln 485	490	495	1488
ttc cag cag cag caa ctg cag atg aac aag atc atc ccc aag cca agc Phe Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser 500	505	510	1536
gag cca gcc cgg cag ccg gag agc cac ccg gag gag acg gag gag gag Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu 515	520	525	1584
ctc cgt gag cac cag gct ctg ctg gac gag ccc tac ctg gac cgg ctg Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu 530	535	540	1632
ccg ggg cag aag gag gcg cac gca cag gcc ggc gtg cag gtg aag cag Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln 545	550	555	1680
gag ccc att gag agc gat gag gaa gag gca gag ccc cca cgg gag gtg Glu Pro Ile Glu Ser Asp Glu Glu Ala Glu Pro Pro Arg Glu Val 565	570	575	1728

gag ccg ggc cag cgc cag ccc agt gag cag gag ctg ctc ttc aga cag Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln 580 585 590	1776
caa gcc ctc ctg ctg gag cag cag cgg atc cac cag ctg agg aac tac Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr 595 600 605	1824
cag gcg tcc atg gag gcc gcc atc ccc gtg tcc ttc ggc ggc cac Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His 610 615 620	1872
agg cct ctg tcc cgg gcg cag tcc tca ccc gcg tct gcc acc ttc ccc Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro 625 630 635 640	1920
gtg tct gtg cag gag ccc acc aag cag agg ttc acg aca ggc ctc Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu 645 650 655	1968
gtg tat gac acg ctg atg ctg aag cac cag tgc acc tgc ggg agt agc Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser 660 665 670	2016
agc agc cac ccc gag cac gcc ggg agg atc cag agc atc tgg tcc cgc Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg 675 680 685	2064
ctg cag gag acg ggc ctc cgg ggc aaa tgc gag tgc atc cgc gga cgc Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg 690 695 700	2112
aag gcc acc ctg gag gag cta cag acg gtg cac tcg gaa gcc cac acc Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr 705 710 715 720	2160
ctc ctg tat ggc acg aac ccc ctc aac cgg cag aaa ctg gac agt aag Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys 725 730 735	2208
aaa ctt cta ggc tcg ctc gcc tcc gtg ttc gtc cgg ctc cct tgc ggt Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly 740 745 750	2256
ggt gtt ggg gtg gac agt gac acc ata tgg aac gag gtg cac tcg cgc Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala 755 760 765	2304
ggg gca gcc cgc ctg gct gtg ggc tgc gtg gta gag ctg gtc ttc aag Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys 770 775 780	2352
gtg gcc aca ggg gag ctg aag aat ggc ttt gct gtg gtc cgc ccc cct Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro 785 790 795 800	2400
gga aag ctt gcg gag gag agc acg ccc atg ggc ttt tgc tac ttc aac Gly Lys Leu Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn 805 810 815	2448

tcc gtg gcc gtg gca gcc aag ctt ctg cag cag agg ttg agc gtg agc Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser 820 825 830	2496
aag atc ctc atc gtg gac tgg gac gtg cac cat gga aac ggg acc cag Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln 835 840 845	2544
cag gct ttc tac agc gac cct agc gtc ctg tac atg tcc ctc cac cgc Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg 850 855 860	2592
tac gac gat ggg aac ttc ttc cca ggc agc ggg gct cct gat gag gtg Tyr Asp Asp Gly Asn Phe Pro Gly Ser Gly Ala Pro Asp Glu Val 865 870 875 880	2640
ggc aca ggg ccc ggc gtg ggt ttc aac gtc aac atg gct ttc acc ggc Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly 885 890 895	2688
ggc ctg gac ccc ccc atg gga gac gct gag tac ttg gcg gcc ttc aga Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg 900 905 910	2736
acg gtg gtc atg ccg atc gcc agc gag ttt gcc ccg gat gtg gtg ctg Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu 915 920 925	2784
gtg tca tca ggc ttc gat gcc gtg gag ggc cac ccc acc cct ctt ggg Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly 930 935 940	2832
ggc tac aac ctc tcc gcc aga tgc ttc ggg tac ctg acg aag cag ctg Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu 945 950 955 960	2880
atg ggc ctg gct ggc ggc att gtc ctg gcc ctc gag gga ggc cac Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His 965 970 975	2928
gac ctg acc gcc att tgc gac gcc tcg gaa gca tgt gtt tct gcc ttg Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu 980 985 990	2976
ctg gga aac gag ctt gat cct ctc cca gaa aag gtt tta cag caa aga Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg 995 1000 1005	3024
ccc aat gca aac gct gtc cgt tcc atg gag aaa gtc atg gag atc cac Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His 1010 1015 1020	3072
agc aag tac tgg cgc tgc ctg cag cgc aca acc tcc aca gcg tct ctg Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg 1025 1030 1035 1040	3120
tct ctg atc gag gct cag act tgc gag aac gaa gaa gcc gag acg gtc Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val 1045 1050 1055	3168
acc gcc atg gcc tcg ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga	3216

Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg
 1060 1065 1070
 cca gat gag gag ccc atg gaa gag gag ccg ccc ctg tag 3255
 Pro Asp Glu Glu Pro Met Glu Glu Pro Pro Leu
 1075 1080

<210> 4
 <211> 1084
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene

<400> 4

Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
 1 5 10 15

Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
 20 25 30

Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
 35 40 45

Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
 50 55 60

Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
 65 70 75 80

Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
 85 90 95

His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
 100 105 110

Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu
 115 120 125

Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu
 130 135 140

Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys
 145 150 155 160

Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln
 165 170 175

Glu Phe Val Leu Asn Lys Lys Ala Leu Ala His Arg Asn Leu Asn
 180 185 190

His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His
 195 200 205

Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser
 210 215 220

Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro
 225 230 235 240
 Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu
 245 250 255
 Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys
 260 265 270
 Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr
 275 280 285
 Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn
 290 295 300
 Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val
 305 310 315 320
 Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg
 325 330 335
 Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro
 340 345 350
 Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala
 355 360 365
 Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg
 370 375 380
 Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser
 385 390 395 400
 Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His
 405 410 415
 Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly
 420 425 430
 Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg
 435 440 445
 Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg
 450 455 460
 Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu
 465 470 475 480
 Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln
 485 490 495
 Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser
 500 505 510
 Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu
 515 520 525
 Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu
 530 535 540
 Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln

545	550	555	560
Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val			
565	570	575	
Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln			
580	585	590	
Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr			
595	600	605	
Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His			
610	615	620	
Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro			
625	630	635	640
Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu			
645	650	655	
Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser			
660	665	670	
Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg			
675	680	685	
Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg			
690	695	700	
Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr			
705	710	715	720
Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys			
725	730	735	
Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly			
740	745	750	
Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala			
755	760	765	
Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys			
770	775	780	
Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro			
785	790	795	800
Gly Lys Leu Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn			
805	810	815	
Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser			
820	825	830	
Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln			
835	840	845	
Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg			
850	855	860	
Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val			
865	870	875	880

Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly
 885 890 895
 Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg
 900 905 910
 Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu
 915 920 925
 Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly
 930 935 940
 Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu
 945 950 955 960
 Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His
 965 970 975
 Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu
 980 985 990
 Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg
 995 1000 1005
 Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His
 1010 1015 1020
 Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg
 1025 1030 1035 1040
 Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val
 1045 1050 1055
 Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg
 1060 1065 1070
 Pro Asp Glu Glu Pro Met Glu Glu Pro Pro Leu
 1075 1080 1084

<210> 5
 <211> 3255
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(3255)
 <223> Dominant negative mutant (H863L) of human histone deacetylase-4
 (HDAC4)
 gene

<400> 5
 atg agc tcc caa agc cat cca gat gga ctt tct ggc cga gac cag cca 48
 Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
 1 5 10 15

gtg gag ctg ctg aat cct gcc cgc gtg aac cac atg ccc agc acg gtg 96
 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
 20 25 30

gat	gtg	gcc	acg	gcf	ctg	cct	ctg	caa	gtg	gcc	ccc	tcg	gca	gtg	ccc	144
Asp	Val	Ala	Thr	Ala	Leu	Pro	Leu	Gln	Val	Ala	Pro	Ser	Ala	Val	Pro	
35					40					45						
atg	gac	ctg	cgf	ctg	gac	cac	cag	tgc	tca	ctg	cct	gtg	gca	gag	ccg	192
Met	Asp	Leu	Arg	Leu	Asp	His	Gln	Phe	Ser	Leu	Pro	Val	Ala	Glu	Pro	
50					55					60						
gcc	ctg	cgg	gag	cag	cag	ctg	cag	cag	gag	ctc	ctg	gcf	ctc	aag	cag	240
Ala	Leu	Arg	Glu	Gln	Gln	Leu	Gln	Glu	Leu	Leu	Ala	Leu	Lys	Gln		
65					70					75			80			
aag	cag	cag	atc	cag	agg	cag	atc	ctc	atc	gct	gag	tgc	cag	agg	cag	288
Lys	Gln	Gln	Ile	Gln	Arg	Gln	Ile	Leu	Ile	Ala	Glu	Phe	Gln	Arg	Gln	
85					90					95						
cac	gag	cag	ctc	tcc	cgf	cag	cac	gag	gcf	cag	ctc	cac	gag	cac	atc	336
His	Glu	Gln	Leu	Ser	Arg	Gln	His	Glu	Ala	Gln	Leu	His	Glu	His	Ile	
100					105					110						
aag	caa	caa	cag	gag	atg	ctg	gcc	atg	aag	cac	cag	cag	gag	ctg	ctg	384
Lys	Gln	Gln	Glu	Met	Leu	Ala	Met	lys	His	Gln	Gln	Glu	Leu	Leu		
115					120					125						
gaa	cac	cag	cgf	aag	ctg	gag	agg	cac	cgc	cag	gag	cag	gag	ctg	gag	432
Glu	His	Gln	Arg	Lys	Leu	Glu	Arg	His	Arg	Gln	Glu	Gln	Glu	Leu	Glu	
130					135					140						
aag	cag	cac	cgg	gag	cag	aag	ctg	cag	cag	ctc	aag	aac	aag	gag	aag	480
Lys	Gln	His	Arg	Glu	Gln	Lys	Leu	Gln	Gln	Leu	Lys	Asn	Lys	Glu	Lys	
145					150					155			160			
ggc	aaa	gag	agt	gcc	gtg	gcc	agc	aca	gaa	gtg	aag	atg	aag	tta	caa	528
Gly	Lys	Glu	Ser	Ala	Val	Ala	Ser	Thr	Glu	Val	Lys	Met	Lys	Leu	Gln	
165					170					175						
gaa	ttt	gtc	ctc	aat	aaa	aag	aag	gcf	ctg	gcc	cac	cgg	aat	ctg	aac	576
Glu	Phe	Val	Leu	Asn	Lys	Lys	Lys	Ala	Leu	Ala	His	Arg	Asn	Leu	Asn	
180					185					190						
cac	tgc	att	tcc	agc	gac	cct	cgc	tac	tgg	tac	ggg	aaa	acg	cag	cac	624
His	Cys	Ile	Ser	Ser	Asp	Pro	Arg	Tyr	Trp	Tyr	Gly	Lys	Thr	Gln	His	
195					200					205						
agt	tcc	ctt	gac	cag	agt	tct	cca	ccc	cag	agc	gga	gtg	tgc	acc	tcc	672
Ser	Ser	Leu	Asp	Gln	Ser	Ser	Pro	Pro	Gln	Ser	Gly	Val	Ser	Thr	Ser	
210					215					220						
tat	aac	cac	ccg	gtc	ctg	gga	atg	tac	gac	gcc	aaa	gat	gac	tgc	cct	720
Tyr	Asn	His	Pro	Val	Leu	Gly	Met	Tyr	Asp	Ala	Lys	Asp	Asp	Phe	Pro	
225					230					235			240			
ctt	agg	aaa	aca	gct	tct	gaa	ccg	aat	ctg	aaa	tta	cgg	tcc	agg	cta	768
Leu	Arg	Lys	Thr	Ala	Ser	Glu	Pro	Asn	Leu	Lys	Leu	Arg	Ser	Arg	Leu	
245					250					255						
aag	cag	aaa	gtg	gcc	gaa	aga	cgf	agc	agc	ccc	ctg	tta	cgc	agg	aaa	816
Lys	Gln	Lys	Val	Ala	Glu	Arg	Arg	Ser	Ser	Pro	Leu	Leu	Arg	Arg	Lys	
260					265					270						

gac ggg cca gtg gtc act gct cta aaa aag cgt ccg ttg gat gtc aca Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr 275 280 285	864
gac tcc gcg tgc agc agc gcc cca ggc tcc gga ccc agc tca ccc aac Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn 290 295 300	912
aac agc tcc ggg agc gtc agc gcg gag aac ggt atc gcg ccc gcc gtc Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val 305 310 315 320	960
ccc agc atc ccg gcg gag acg agt ttg gcg cac aga ctt gtg gca cga Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg 325 330 335	1008
gaa ggc tcg gcc gct cca ctt ccc ctc tac aca tcg cca tcc ttg ccc Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro 340 345 350	1056
aac atc acg ctg ggc ctg cct gcc acc ggc ccc tct gcg ggc acg gcg Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala 355 360 365	1104
ggc cag cag gac acc gag aga ctc acc ctt ccc gcc ctc cag cag agg Gly Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg 370 375 380	1152
ctc tcc ctt ttc ccc ggc acc cac ctc act ccc tac ctg agc acc tcg Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser 385 390 395 400	1200
ccc ttg gag cgg gac gga ggg gca gcg cac agc cct ctt ctg cag cac Pro Leu Glu Arg Asp Gly Ala Ala His Ser Pro Leu Leu Gln His 405 410 415	1248
atg gtc tta ctg gag cag cca ccg gca caa gca ccc ctc gtc aca ggc Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly 420 425 430	1296
ctg gga gca ctg ccc ctc cac gca cag tcc ttg gtt ggt gca gac cgg Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg 435 440 445	1344
gtg tcc ccc tcc atc cac aag ctg cgg cag cac cgc cca ctg ggg cgg Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg 450 455 460	1392
acc cag tcg gcc ccg ctg ccc cag aac gcc cag gct ctg cag cac ctg Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu 465 470 475 480	1440
gtc atc cag cag cag cat cag cag ttt ctg gag aaa cac aag cag cag Val Ile Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln 485 490 495	1488
ttc cag cag cag caa ctg cag atg aac aag atc atc ccc aag cca agc Phe Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser 500 505 510	1536
gag cca gcc cgg cag ccg gag agc cac ccg gag gag acg gag gag gag 515 520 525 530	1584

Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu			
515	520	525	
ctc cgt gag cac cag gct ctg ctg gac gag ccc tac ctg gac cgg ctg			1632
Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu			
530	535	540	
ccg ggg cag aag gag gcg cac gca cag gcc ggc gtg cag gtg aag cag			1680
Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln			
545	550	555	560
gag ccc att gag agc gat gag gaa gag gca gag ccc cca cgg gag gtg			1728
Glu Pro Ile Glu Ser Asp Glu Glu Ala Glu Pro Pro Arg Glu Val			
565	570	575	
gag ccg ggc cag cgc cag ccc agt gag cag gag ctg ctc ttc aga cag			1776
Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln			
580	585	590	
caa gcc ctc ctg ctg gag cag cag cgg atc cac cag ctg agg aac tac			1824
Gln Ala Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr			
595	600	605	
cag gcg tcc atg gag gcc gcc atc ccc gtg tcc ttc ggc ggc cac			1872
Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His			
610	615	620	
agg cct ctg tcc cgg gcg cag tcc tca ccc gcg tct gcc acc ttc ccc			1920
Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro			
625	630	635	640
gtg tct gtg cag gag ccc ccc acc aag ccg agg ttc acg aca ggc ctc			1968
Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu			
645	650	655	
gtg tat gac acg ctg atg ctg aag cac cag tgc acc tgc ggg agt agc			2016
Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser			
660	665	670	
agc agc cac ccc gag cac gcc ggg agg atc cag agc atc tgg tcc cgc			2064
Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg			
675	680	685	
ctg cag gag acg ggc ctc cgg ggc aaa tgc gag tgc atc cgc gga cgc			2112
Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg			
690	695	700	
aag gcc acc ctg gag gag cta cag acg gtg cac tcg gaa gcc cac acc			2160
Lys Ala Thr Leu Glu Leu Gln Thr Val His Ser Glu Ala His Thr			
705	710	715	720
ctc ctg tat ggc acg aac ccc ctc aac cgg cag aaa ctg gac agt aag			2208
Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys			
725	730	735	
aaa ctt cta ggc tcg ctc gcc tcc gtg ttc gtc cgg ctc cct tgc ggt			2256
Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly			
740	745	750	
ggt gtt ggg gtg gac agt gac acc ata tgg aac gag gtg cac tcg gcg			2304
Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala			

755	760	765	
ggg gca gcc cgc ctg gct gtg ggc tgc gtg gta gag ctg gtc ttc aag Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys 770	775	780	2352
gtg gcc aca ggg gag ctg aag aat ggc ttt gct gtg gtc cgc ccc cct Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro 785	790	795	2400
gga cac cat gcg gag gag agc acg ccc atg ggc ttt tgc tac ttc aac Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn 805	810	815	2448
tcc gtg gcc gtg gca gcc aag ctt ctg cag cag agg ttg agc gtg agc Ser Val Ala Val Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser 820	825	830	2496
aag atc ctc atc gtg gac tgg gac gtg cac cat gga aac ggg acc cag Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln 835	840	845	2544
cag gct ttc tac agc gac cct agc gtc ctg tac atg tcc ctc ctt cgc Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu Leu Arg 850	855	860	2592
tac gac gat ggg aac ttc ttc cca ggc agc ggg gct cct gat gag gtg Tyr Asp Asp Gly Asn Phe Pro Gly Ser Gly Ala Pro Asp Glu Val 865	870	875	2640
880			
ggc aca ggg ccc ggc gtg ggt ttc aac gtc aac atg gct ttc acc ggc Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly 885	890	895	2688
ggc ctg gac ccc ccc atg gga gac gct gag tac ttg gcg gcc ttc aga Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg 900	905	910	2736
915			
acg gtg gtc atg ccg atc gcc agc gag ttt gcc ccg gat gtg gtg ctg Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu 920	925		2784
930			
gtg tca tca ggc ttc gat gcc gtg gag ggc cac ccc acc cct ctt ggg Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly 935	940		2832
945			
ggc tac aac ctc tcc gcc aga tgc ttc ggg tac ctg acg aag cag ctg Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu 950	955	960	2880
965			
atg ggc ctg gct ggc ggc cgg att gtc ctg gcc ctc gag gga ggc cac Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His 970	975		2928
980			
gac ctg acc gcc att tgc gac gcc tcg gaa gca tgt gtt tct gcc ttg Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu 985	990		2976
995			
ctg gga aac gag ctt gat cct ctc cca gaa aag gtt tta cag caa aga Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg 1000	1005		3024

ccc aat gca aac gct gtc cgt tcc atg gag aaa gtc atg gag atc cac	3072
Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His	
1010 1015 1020	
agc aag tac tgg cgc tgc ctg cag cgc aca acc tcc aca gcg ggg cgt	3120
Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg	
1025 1030 1035 1040	
tct ctg atc gag gct cag act tgc gag aac gaa gaa gcc gag acg gtc	3168
Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Ala Glu Thr Val	
1045 1050 1055	
acc gcc atg gcc tcg ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga	3216
Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg	
1060 1065 1070	
cca gat gag gag ccc atg gaa gag gag ccg ccc ctg tag	3255
Pro Asp Glu Glu Pro Met Glu Glu Pro Pro Leu	
1075 1080	

<210> 6
 <211> 1084
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Dominant negative mutant (H863L) of human histone deacetylase-4
 (HDAC4)
 gene

<400> 6

Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro	
1 5 10 15	
Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val	
20 25 30	
Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro	
35 40 45	
Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro	
50 55 60	
Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln	
65 70 75 80	
Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln	
85 90 95	
His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile	
100 105 110	
Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu	
115 120 125	
Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu	
130 135 140	

Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys
 145 150 155 160
 Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln
 165 170 175
 Glu Phe Val Leu Asn Lys Lys Ala Leu Ala His Arg Asn Leu Asn
 180 185 190
 His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His
 195 200 205
 Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser
 210 215 220
 Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro
 225 230 235 240
 Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu
 245 250 255
 Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys
 260 265 270
 Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr
 275 280 285
 Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn
 290 295 300
 Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val
 305 310 315 320
 Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg
 325 330 335
 Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro
 340 345 350
 Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala
 355 360 365
 Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg
 370 375 380
 Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser
 385 390 395 400
 Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His
 405 410 415
 Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly
 420 425 430
 Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg
 435 440 445
 Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg
 450 455 460
 Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu

465	470	475	480
Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln			
485	490	495	
Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser			
500	505	510	
Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu			
515	520	525	
Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu			
530	535	540	
Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln			
545	550	555	560
Glu Pro Ile Glu Ser Asp Glu Glu Ala Glu Pro Pro Arg Glu Val			
565	570	575	
Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln			
580	585	590	
Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr			
595	600	605	
Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His			
610	615	620	
Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro			
625	630	635	640
Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu			
645	650	655	
Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser			
660	665	670	
Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg			
675	680	685	
Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg			
690	695	700	
Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr			
705	710	715	720
Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys			
725	730	735	
Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly			
740	745	750	
Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala			
755	760	765	
Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys			
770	775	780	
Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro			
785	790	795	800

Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn
 805 810 815
 Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser
 820 825 830
 Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln
 835 840 845
 Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu Leu Arg
 850 855 860
 Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val
 865 870 875 880
 Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly
 885 890 895
 Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg
 900 905 910
 Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu
 915 920 925
 Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly
 930 935 940
 Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu
 945 950 955 960
 Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His
 965 970 975
 Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu
 980 985 990
 Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg
 995 1000 1005
 Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His
 1010 1015 1020
 Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg
 1025 1030 1035 1040
 Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val
 1045 1050 1055
 Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg
 1060 1065 1070
 Pro Asp Glu Glu Pro Met Glu Glu Pro Pro Leu
 1075 1080 1084

<210> 7
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (43)..(1176)
 <223> human histone deacetylase-8 (HDAC8) gene

<400> 7
 gccagatctg gaaggtggct gcggAACGGT tttaAGCGGA AG ATG GAG GAG CCG 54
 Met Glu Glu Pro
 1

gag gaa ccg gcg gac agt ggg cag tcg ctg gtc ccg gtt tat atc tat 102
 Glu Glu Pro Ala Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr
 5 10 15 20

agt ccc gag tat gtc agt atg tgt gac tcc ctg gcc aag atc ccc aaa 150
 Ser Pro Glu Tyr Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys
 25 30 35

cgg gcc agt atg gtg cat tct ttg att gaa gca tat gca ctg cat aag 198
 Arg Ala Ser Met Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys
 40 45 50

cag atg agg ata gtt aag cct aaa gtg gcc tcc atg gag gag atg gcc 246
 Gln Met Arg Ile Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala
 55 60 65

acc ttc cac act gat gct tat ctg cag cat ctc cag aag gtc agc caa 294
 Thr Phe His Thr Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln
 70 75 80

gag ggc gat gat gat cat ccg gac tcc ata gaa tat ggg cta ggt tat 342
 Glu Gly Asp Asp Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr
 85 90 95 100

gac tgc cca gcc act gaa ggg ata ttt gac tat gca gca gct ata gga 390
 Asp Cys Pro Ala Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ile Gly
 105 110 115

ggg gct acg atc aca gct gcc caa tgc ctg att gac gga atg tgc aaa 438
 Gly Ala Thr Ile Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys
 120 125 130

gta gca att aac tgg tct gga ggg tgg cat cat gca aag aaa gat gaa 486
 Val Ala Ile Asn Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu
 135 140 145

gca tct ggt ttt tgt tat ctc aat gat gct gtc ctg gga ata tta cga 534
 Ala Ser Gly Phe Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg
 150 155 160

ttg cga cgg aaa ttt gag cgt att ctc tac gtg gat ttg gat ctg cac 582
 Leu Arg Arg Lys Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His
 165 170 175 180

cat gga gat ggt gta gaa gac gca ttc agt ttc acc tcc aaa gtc atg 630
 His Gly Asp Gly Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met
 185 190 195

acc gtg tcc ctg cac aaa ttc tcc cca gga ttt ttc cca gga aca ggt 678
 Thr Val Ser Leu His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly
 200 205 210

gac gtg tct gat gtt ggc cta ggg aag gga cgg tac tac agt gta aat Asp Val Ser Asp Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn 215 220 225	726
gtg ccc att cag gat ggc ata caa gat gaa aaa tat tac cag atc tgt Val Pro Ile Gln Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gin Ile Cys 230 235 240	774
gaa agt gta cta aag gaa gta tac caa gcc ttt aat ccc aaa gca gtg Glu Ser Val Leu Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val 245 250 255 260	822
gtc tta cag ctg gga gct gac aca ata gct ggg gat ccc atg tgc tcc Val Leu Gln Leu Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser 265 270 275	870
ttt aac atg act cca gtg gga att ggc aag tgt ctt aag tac atc ctt Phe Asn Met Thr Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu 280 285 290	918
caa tgg cag ttg gca aca ctc att ttg gga gga gga ggc tat aac ctt Gln Trp Gln Leu Ala Thr Leu Ile Leu Gly Gly Gly Tyr Asn Leu 295 300 305	966
gcc aac acg gct cga tgc tgg aca tac ttg acc ggg gtc atc cta ggg Ala Asn Thr Ala Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly 310 315 320	1014
aaa aca cta tcc tct gag atc cca gat cat gag ttt ttc aca gca tat Lys Thr Leu Ser Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr 325 330 335 340	1062
ggt cct gat tat gtg ctg gaa atc acg cca agc tgc cgg cca gac cgc Gly Pro Asp Tyr Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg 345 350 355	1110
aat gag ccc cac cga atc caa caa atc ctc aac tac atc aaa ggg aat Asn Glu Pro His Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn 360 365 370	1158
ctg aag cat gtg gtc tag ttgacagaaaa gagatcaggt ttccagagct Leu Lys His Val Val 375	1206
gaggagtggt gcctataatg aagacagcgt gtttatgcaa gcagtttgtg gaatttgtga	1266
ctgcagggaa aatttgaagaa aaattacttc ctgaaaattt ccaaggggca tcaagtggca	1326
gctggcttcc tgggggtgaag aggcaggcac cccagagtc tcaactggac cttagggaaag	1386
aaggagatat cccacattta aagttcttat ttaaaaaaaaac acacacacac aaatgaaatt	1446
tttaatcttt gaaaatttatt tttaagcgaa ttggggaggg gagtattttta atcatcttaa	1506
atgaaacaga tcagaagctg gatgagagca gtcaccagtt tgttagggcag gaggcagctg	1566
agaggcaggg tttgggcctc aggaccatcc aggtggagcc ctgggagaga gggtaactgat	1626
cagcagactg ggaggtgggg agaagtccgc tgggtttgtt ttagtgttat atatcttgg	1686

tttttttaat aaaatcttg aaaacctaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1743

<210> 8
<211> 377
<212> PRT
<213> Homo sapiens

<400> 8
Met Glu Glu Pro Glu Glu Pro Ala Asp Ser Gly Gln Ser Leu Val Pro
1 5 10 15

Val Tyr Ile Tyr Ser Pro Glu Tyr Val Ser Met Cys Asp Ser Leu Ala
20 25 30

Lys Ile Pro Lys Arg Ala Ser Met Val His Ser Leu Ile Glu Ala Tyr
35 40 45

Ala Leu His Lys Gln Met Arg Ile Val Lys Pro Lys Val Ala Ser Met
50 55 60

Glu Glu Met Ala Thr Phe His Thr Asp Ala Tyr Leu Gln His Leu Gln
65 70 75 80

Lys Val Ser Gln Glu Gly Asp Asp Asp His Pro Asp Ser Ile Glu Tyr
85 90 95

Gly Leu Gly Tyr Asp Cys Pro Ala Thr Glu Gly Ile Phe Asp Tyr Ala
100 105 110

Ala Ala Ile Gly Gly Ala Thr Ile Thr Ala Ala Gln Cys Leu Ile Asp
115 120 125

Gly Met Cys Lys Val Ala Ile Asn Trp Ser Gly Gly Trp His His Ala
130 135 140

Lys Lys Asp Glu Ala Ser Gly Phe Cys Tyr Leu Asn Asp Ala Val Leu
145 150 155 160

Gly Ile Leu Arg Leu Arg Arg Lys Phe Glu Arg Ile Leu Tyr Val Asp
165 170 175

Leu Asp Leu His His Gly Asp Gly Val Glu Asp Ala Phe Ser Phe Thr
180 185 190

Ser Lys Val Met Thr Val Ser Leu His Lys Phe Ser Pro Gly Phe Phe
195 200 205

Pro Gly Thr Gly Asp Val Ser Asp Val Gly Leu Gly Lys Gly Arg Tyr
210 215 220 220

Tyr Ser Val Asn Val Pro Ile Gln Asp Gly Ile Gln Asp Glu Lys Tyr
225 230 235 240

Tyr Gln Ile Cys Glu Ser Val Leu Lys Glu Val Tyr Gln Ala Phe Asn
245 250 255

Pro Lys Ala Val Val Leu Gln Leu Gly Ala Asp Thr Ile Ala Gly Asp
260 265 270

Pro Met Cys Ser Phe Asn Met Thr Pro Val Gly Ile Gly Lys Cys Leu
275 280 285

Lys Tyr Ile Leu Gln Trp Gln Leu Ala Thr Leu Ile Leu Gly Gly Gly
290 295 300

Gly Tyr Asn Leu Ala Asn Thr Ala Arg Cys Trp Thr Tyr Leu Thr Gly
305 310 315 320

Val Ile Leu Gly Lys Thr Leu Ser Ser Glu Ile Pro Asp His Glu Phe
325 330 335

Phe Thr Ala Tyr Gly Pro Asp Tyr Val Leu Glu Ile Thr Pro Ser Cys
340 345 350

Arg Pro Asp Arg Asn Glu Pro His Arg Ile Gln Gln Ile Leu Asn Tyr
355 360 365

Ile Lys Gly Asn Leu Lys His Val Val
370 375

<210> 9
<211> 1449
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1449)
<223> human histone deacetylase-1 (HDAC1) gene

<400> 9
atg gcg cag acg cag ggc acc cgg agg aaa gtc tgt tac tac tac gac 48
Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Asp
1 5 10 15

ggg gat gtt gga aat tac tat tat gga caa ggc cac cca atg aag cct 96
Gly Asp Val Gly Asn Tyr Tyr Gly Gln Gly His Pro Met Lys Pro

20

25

30

cac cga atc cgc atg act cat aat ttg ctg ctc aac tat ggt ctc tac			144
His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr			
35	40	45	
cga aaa atg gaa atc tat cgc cct cac aaa gcc aat gct gag gag atg			192
Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met			
50	55	60	
acc aag tac cac agc gat gac tac att aaa ttc ttg cgc tcc atc cgt			240
Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg			
65	70	75	80
cca gat aac atg tcg gag tac agc aag cag atg cag aca ttc aac gtt			288
Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val			
85	90	95	
ggt gag gac tgt cca gta ttc gat ggc ctg ttt gag ttc tgt cag ttg			336
Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu			
100	105	110	
tct act ggt ggt tct gtg gca agt gct gtg aaa ctt aat aag cag cag			384
Ser Thr Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln			
115	120	125	
acg gac atc gct gtg aat tgg gct ggg ggc ctg cac cat gca aag aag			432
Thr Asp Ile Ala Val Asn Trp Ala Gly Leu His His Ala Lys Lys			
130	135	140	
tcc gag gca tct ggc ttc tgt tac gtc aat gat atc gtc ttg gcc atc			480
Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile			
145	150	155	160
ctg gaa ctg cta aag tat cac cag agg gtg ctg tac att gac att gat			528
Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp			
165	170	175	
att cac cat ggt gac ggc gtg gaa gag gcc ttc tac acc acg gac cgg			576
Ile His His Asp Gly Val Glu Ala Phe Tyr Thr Thr Asp Arg			
180	185	190	
gtc atg act gtg tcc ttt cat aag tat gga gag tac ttc cca gga act			624
Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr			
195	200	205	
ggg gac cta cgg gat atc ggg gct ggc aaa ggc aag tat tat gct gtt			672
Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val			
210	215	220	
aac tac ccc ctc cga gac ggg att gat gac gag tcc tat gag gcc att			720
Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile			
225	230	235	240
ttc aag ccc gtc atg tcc aaa gta atg gag atg ttc cag cct agt gcg			768
Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala			
245	250	255	
gtg gtc tta cag tgt ggc tca gac tcc cta tct ggg gat cgg tta ggt			816
Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly			
260	265	270	

tgc ttc aat cta act atc aaa gga cac gcc aag tgt gtg gaa ttt gtc Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val 275 280 285	864
aag agc ttt aac ctg cct atg ctg atg ctg gga ggc ggt ggt tac acc Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr 290 295 300	912
att cgt aac gtt gcc cgg tgc agg aca tat gag aca gct gtg gcc ctg Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu 305 310 315 320	960
gat acg gag atc cct aat gag ctt cca tac aat gac tac ttt gaa tac Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr 325 330 335	1008
ttt gga cca gat ttc aag ctc cac atc agt cct tcc aat atg act aac Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn 340 345 350	1056
cag aac acg aat gag tac ctg gag aag atc aaa cag cga ctg ttt gag Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu 355 360 365	1104
aac ctt aga atg ctg ccg cac gca cct ggg gtc caa atg cag gcg att Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile 370 375 380	1152
cct gag gac gcc atc cct gag gag agt ggc gat gag gac gaa gac gac Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp 385 390 395 400	1200
cct gac aag cgc atc tcg atc tgc tcc tct gac aaa cga att gcc tgt Pro Asp Lys Arg Ile Ser Ile Cys Ser Asp Lys Arg Ile Ala Cys 405 410 415	1248
gag gaa gag ttc tcc gat tct gaa gag gag gga gag ggg ggc cgc aag Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Arg Lys 420 425 430	1296
aac tct tcc aac ttc aaa aaa gcc aag aga gtc aaa aca gag gat gaa Asn Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu 435 440 445	1344
aaa gag aaa gac cca gag gag aag aaa gaa gtc acc gaa gag gag aaa Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys 450 455 460	1392
acc aag gag gag aag cca gaa gcc aaa ggg gtc aag gag gag gtc aag Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys 465 470 475 480	1440
ttg gcc tga Leu Ala	1449

<210> 10
<211> 482
<212> PRT

<213> Homo sapiens

<400> 10
Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
1 5 10 15

Gly Asp Val Gly Asn Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
20 25 30

His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
35 40 45

Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
50 55 60

Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
65 70 75 80

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
85 90 95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
100 105 110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
115 120 125

Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys
130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
145 150 155 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
165 170 175

Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg
180 185 190

Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr
195 200 205

Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
210 215 220

Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile
225 230 235 240

Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala
245 250 255

Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly
260 265 270

Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val
275 280 285

Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr
290 295 300

Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu
305 310 315 320

Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr
325 330 335

Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn
340 345 350

Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu
355 360 365

Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile
370 375 380

Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp
385 390 395 400

Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys
405 410 415

Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Arg Lys
420 425 430

Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu
435 440 445

Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys
450 455 460

Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys
465 470 475 480

Leu Ala

<210> 11
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1449)
<223> Dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 11
atg gcg cag acg cag ggc acc cgg agg aaa gtc tgt tac tac tac gac 48
Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
1 5 10 15

ggg gat gtt gga aat tac tat tat gga caa ggc cac cca atg aag cct 96
Gly Asp Val Gly Asn Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
20 25 30

cac cga atc cgc atg act cat aat ttg ctg ctc aac tat ggt ctc tac 144
His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
35 40 45

cga aaa atg gaa atc tat cgc cct cac aaa gcc aat gct gag gag atg 192
Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
50 55 60

acc aag tac cac agc gat gac tac att aaa ttc ttg cgc tcc atc cgt 240
Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
65 70 75 80

cca gat aac atg tcg gag tac agc aag cag atg cag aga ttc aac gtt 288
Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
85 90 95

ggg gag gac tgt cca gta ttc gat ggc ctg ttt gag ttc tgt cag ttg 336
Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
100 105 110

tct act ggt ggt tct gtg gca agt gct gtg aaa ctt aat aag cag cag 384
Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
115 120 125

acg gac atc gct gtg aat tgg gct ggg ggc ctg aag ctt gca aag aag 432
Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys
130 135 140

tcc gag gca tct ggc ttc tgt tac gtc aat gat atc gtc ttg gcc atc 480
Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
145 150 155 160

ctg gaa ctg cta aag tat cac cag agg gtg ctg tac att gac att gat 528
Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
165 170 175

att cac cat ggt gac ggc gtg gaa gag gcc ttc tac acc acg gac cgg Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg 180 185 190	576
gtc atg act gtg tcc ttt cat aag tat gga gag tac ttc cca gga act Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr 195 200 205	624
ggg gac cta cgg gat atc ggg gct ggc aaa ggc aag tat tat gct gtt Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Tyr Tyr Ala Val 210 215 220	672
aac tac ccg ctc cga gac ggg att gat gac gag tcc tat gag gcc att Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile 225 230 235 240	720
ttc aag ccg gtc atg tcc aaa gta atg gag atg ttc cag cct agt gcg Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala 245 250 255	768
gtg gtc tta cag tgt ggc tca gac tcc cta tct ggg gat cgg tta ggt Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly 260 265 270	816
tgc ttc aat cta act atc aaa gga cac gcc aag tgt gtg gaa ttt gtc Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val 275 280 285	864
aag agc ttt aac ctg cct atg ctg atg ctg gga ggc ggt ggt tac acc Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr 290 295 300	912
att cgt aac gtt gcc cgg tgc agg aca tat gag aca gct gtg gcc ctg Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu 305 310 315 320	960
gat acg gag atc cct aat gag ctt cca tac aat gac tac ttt gaa tac Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr 325 330 335	1008
ttt gga cca gat ttc aag ctc cac atc agt cct tcc aat atg act aac Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn 340 345 350	1056
cag aac acg aat gag tac ctg gag aag atc aaa cag cga ctg ttt gag Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu 355 360 365	1104
aac ctt aga atg ctg ccg cac gca cct ggg gtc caa atg cag gcg att Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile 370 375 380	1152
cct gag gac gcc atc cct gag gag agt ggc gat gag gac gaa gac gac Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp 385 390 395 400	1200
cct gac aag cgc atc tcg atc tgc tcc tct gac aaa cga att gcc tgt Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys 405 410 415	1248
gag gaa gag ttc tcc gat tct gaa gag gag gga gac ggg ggc cgc aag	1296

Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys			
420	425	430	
aac tct tcc aac ttc aaa aaa gcc aag aga gtc aaa aca gag gat gaa			1344
Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu			
435	440	445	
aaa gag aaa gac cca gag gag aag aaa gaa gtc acc gaa gag gag aaa			1392
Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys			
450	455	460	
acc aag gag gag aag cca gaa gcc aaa ggg gtc aag gag gag gtc aag			1440
Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys			
465	470	475	480
ttg gcc tga			1449
Leu Ala			
<210> 12			
<211> 482			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene			
<400> 12			
Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp			
1	5	10	15
Gly Asp Val Gly Asn Tyr Tyr Gly Gln Gly His Pro Met Lys Pro			
20	25	30	
His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr			
35	40	45	
Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met			
50	55	60	
Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg			
65	70	75	80
Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val			
85	90	95	
Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu			
100	105	110	
Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln			
115	120	125	

Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys
130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
145 150 155 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
165 170 175

Ile His His Gly Asp Gly Val Glu Ala Phe Tyr Thr Thr Asp Arg
180 185 190

Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr
195 200 205

Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
210 215 220

Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile
225 230 235 240

Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala
245 250 255

Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly
260 265 270

Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val
275 280 285

Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr
290 295 300

Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu
305 310 315 320

Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr
325 330 335

Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn
340 345 350

Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu
355 360 365

Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile
370 375 380

Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp
385 390 395 400

Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys
405 410 415

Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Arg Lys
420 425 430

Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu
435 440 445

Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys
450 455 460

Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys
465 470 475 480

Leu Ala

<210> 13
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1449)
<223> Dominant negative mutant (H199L) of human histone deacetylase-1
(HDAC1)
gene

<400> 13
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Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
1 5 10 15

ggg gat gtt gga aat tac tat tat gga caa ggc cac cca atg aag cct 96
Gly Asp Val Gly Asn Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
20 25 30

cac cga atc cgc atg act cat aat ttg ctg ctc aac tat ggt ctc tac 144
His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
35 40 45

cga aaa atg gaa atc tat cgc cct cac aaa gcc aat gct gag gag atg 192
Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
50 55 60

acc aag tac cac agc gat gac tac att aaa ttc ttg cgc tcc atc cgt	240
Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg	
65 70 75 80	
cca gat aac atg tcg gag tac agc aag cag atg cag aga ttc aac gtt	288
Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val	
85 90 95	
ggt gag gac tgt cca gta ttc gat ggc ctg ttt gag ttc tgt cag ttg	336
Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu	
100 105 110	
tct act ggt ggt tct gtg gca agt gct gtg aaa ctt aat aag cag cag	384
Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln	
115 120 125	
acg gac atc gct gtg aat tgg gct ggg ggc ctg cac cat gca aag aag	432
Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys	
130 135 140	
tcc gag gca tct ggc ttc tgt tac gtc aat gat atc gtc ttg gcc atc	480
Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile	
145 150 155 160	
ctg gaa ctg cta aag tat cac cag agg gtg ctg tac att gac att gat	528
Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp	
165 170 175	
att cac cat ggt gac ggc gtg gaa gag gcc ttc tac acc acg gac cgg	576
Ile His His Gly Asp Gly Val Glu Ala Phe Tyr Thr Thr Asp Arg	
180 185 190	
gtc atg act gtg tcc ttt ctt aag tat gga gag tac ttc cca gga act	624
Val Met Thr Val Ser Phe Leu Lys Tyr Gly Glu Tyr Phe Pro Gly Thr	
195 200 205	
ggg gac cta cgg gat atc ggg gct ggc aaa ggc aag tat tat gct gtt	672
Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val	
210 215 220	
aac tac ccg ctc cga gac ggg att gat gac gag tcc tat gag gcc att	720
Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile	
225 230 235 240	
ttc aag ccg gtc atg tcc aaa gta atg gag atg ttc cag cct agt gcg	768
Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala	
245 250 255	
gtg gtc tta cag tgt ggc tca gac tcc cta tct ggg gat cgg tta ggt	816
Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly	
260 265 270	
tgc ttc aat cta act atc aaa gga cac gcc aag tgt gtg gaa ttt gtc	864
Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val	
275 280 285	
aag agc ttt aac ctg cct atg ctg atg ctg gga ggc ggt ggt tac acc	912
Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr	
290 295 300	
att cgt aac gtt gcc cgg tgc agg aca tat gag aca gct gtg gcc ctg	960

Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu				
305	310	315	320	
gat acg gag atc cct aat gag ctt cca tac aat gac tac ttt gaa tac				1008
Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr				
325	330	335		
ttt gga cca gat ttc aag ctc cac atc agt cct tcc aat atg act aac				1056
Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn				
340	345	350		
cag aac acg aat gag tac ctg gag aag atc aaa cag cga ctg ttt gag				1104
Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu				
355	360	365		
aac ctt aga atg ctg ccg cac gca cct ggg gtc caa atg cag gcg att				1152
Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile				
370	375	380		
cct gag gac gcc atc cct gag gag agt ggc gat gag gac gaa gac gac				1200
Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp				
385	390	395	400	
cct gac aag cgc atc tcg atc tgc tcc tct gac aaa cga att gcc tgt				1248
Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys				
405	410	415		
gag gaa gag ttc tcc gat tct gaa gag gag gga gag ggg ggc cgc aag				1296
Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Arg Lys				
420	425	430		
aac tct tcc aac ttc aaa aaa gcc aag aga gtc aaa aca gag gat gaa				1344
Asn Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu				
435	440	445		
aaa gag aaa gac cca gag gag aag aaa gaa gtc acc gaa gag gag aaa				1392
Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys				
450	455	460		
acc aag gag gag aag cca gaa gcc aaa ggg gtc aag gag gag gtc aag				1440
Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys				
465	470	475	480	
ttg gcc tga				1449
Leu Ala				

<210> 14
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> Dominant negative mutant (H199L) of human histone deacetylase-1
(HDAC1)
gene

<400> 14
Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
1 5 10 15

Gly Asp Val Gly Asn Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
20 25 30

His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
35 40 45

Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
50 55 60

Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
65 70 75 80

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
85 90 95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
100 105 110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
115 120 125

Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys
130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
145 150 155 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
165 170 175

Ile His His Gly Asp Gly Val Glu Ala Phe Tyr Thr Thr Asp Arg
180 185 190

Val Met Thr Val Ser Phe Leu Lys Tyr Gly Glu Tyr Phe Pro Gly Thr
195 200 205

Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
210 215 220

Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile
225 230 235 240

Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala
245 250 255

Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly
260 265 270

Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val
275 280 285

Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr
290 295 300

Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu
305 310 315 320

Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr
325 330 335

Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn
340 345 350

Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu
355 360 365

Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile
370 375 380

Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp
385 390 395 400

Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys
405 410 415

Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Arg Lys
420 425 430

Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu
435 440 445

Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys
450 455 460

Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys
465 470 475 480

Leu Ala

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<210> 15
<211> 1287
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1287)
<223> human histone deacetylase-3 (HDAC3) gene

<400> 15
atg gcc aag acc gtc gcc tat ttc tac gac ccc gac gtc ggc aac ttc      48
Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
1           5           10           15

cac tac gga gct gga cac cct atg aag ccc cat cgc ctg gca ttg acc      96
His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
20          25          30

cat agc ctg gtc ctg cat tac ggt ctc tat aag aag atg atc gtc ttc      144
His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
35          40          45

aag cca tac cag gcc tcc caa cat gac atg tgc cgc ttc cac tcc gag      192
Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
50          55          60

gac tac att gac ttc ctg cag aga gtc agc ccc acc aat atg caa ggc      240
Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
65          70          75          80

ttc acc aag agt ctt aat gcc ttc aac gta ggc gat gac tgc cca gtg      288
Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
85          90          95

ttt ccc ggg ctc ttt gag ttc tgc tcg cgt tac aca ggc gca tct ctg      336
Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
100         105         110

caa gga gca acc cag ctg aac aac aag atc tgt gat att gcc att aac      384
Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
115         120         125

tgg gct ggt ggt ctg cac cat gcc aag aag ttt gag gcc tct ggc ttc      432
Trp Ala Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe
130         135         140

tgc tat gtc aac gac att gtc att ggc atc ctg gag ctg ctc aag tac      480
Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
145         150         155         160

cac cct cgg gtc ctc tac att gac att gac atc cac cat ggt gac ggg      528
His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
165         170         175

gtt caa gaa gct ttc tac ctc act gac cgg gtc atg acg gtc tcc ttc      576
Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe
180         185         190

cac aaa tac gga aat tac ttc ttc cct ggc aca ggt gac atg tat gaa      624
His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu

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195	200	205	
gtc ggg gca gag agt ggc cgc tac tac tgt ctg aac gtg ccc ctg cgg Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg	210	215	672
gat ggc att gat gac cag agt tac aag cac ctt ttc cag ccg gtt atc Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile	225	230	720
aac cag gta gtg gac ttc tac caa ccc acg tgc att gtg ctc cag tgt Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys	245	250	768
gga gct gac tct ctg ggc tgt gat cga ttg ggc tgc ttt aac ctc agc Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser	260	265	816
atc cga ggg cat ggg gaa tgc gtt gaa tat gtc aag agc ttc aat atc Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile	275	280	864
cct cta ctc gtg ctg ggt ggt ggt tat act gtc cga aat gtt gcc Pro Leu Leu Val Leu Gly Gly Gly Tyr Thr Val Arg Asn Val Ala	290	295	912
cgc tgc tgg aca tat gag aca tcg ctg ctg gta gaa gag gcc att agt Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser	305	310	960
gag gag ctt ccc tat agt gaa tac ttc gag tac ttt gcc cca gac ttc Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe	325	330	1008
aca ctt cat cca gat gtc agc acc cgc atc gag aat cag aac tca cgc Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg	340	345	1056
cag tat ctg gac cag atc ctc cag aca atc ttt gaa aac ctg aag atg Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met	355	360	1104
ctg aac cat gca cct agt gtc cag att cat gac gtg cct gca gac ctc Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu	370	375	1152
ctg acc tat gac agg act gat gag gct gat gca gag gag agg ggt cct Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro	385	390	1200
gag gag aac tat agc agg cca gag gca ccc aat gag ttc tat gat gga Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly	405	410	1248
gac cat gac aat gac aag gaa agc gat gtg gag att taa Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile	420	425	1287

<210> 16
<211> 428

<212> PRT

<213> Homo sapiens

<400> 16

Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
1 5 10 15

His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
20 25 30

His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
35 40 45

Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
50 55 60

Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
65 70 75 80

Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
85 90 95

Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
100 105 110

Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
115 120 125

Trp Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe
130 135 140

Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
145 150 155 160

His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
165 170 175

Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe
180 185 190

His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu
195 200 205

Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg
210 215 220

Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile

225

230

235

240

Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys
245 250 255

Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser
260 265 270

Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile
275 280 285

Pro Leu Leu Val Leu Gly Gly Gly Tyr Thr Val Arg Asn Val Ala
290 295 300

Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser
305 310 315 320

Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe
325 330 335

Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg
340 345 350

Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met
355 360 365

Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu
370 375 380

Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro
385 390 395 400

Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly
405 410 415

Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile
420 425

<210> 17

<211> 1287

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1287)

<223> Dominant negative mutant (H134K, H135L) of human histone deacetylase-3
(HDAC3) gene

<400> 17			
atg gcc aag acc gtc gcc tat ttc tac gac ccc gac gtc ggc aac ttc			48
Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe			
1 5 10 15			
cac tac gga gct gga cac cct atg aag ccc cat cgc ctg gca ttg acc			96
His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr			
20 25 30			
cat agc ctg gtc ctg cat tac ggt ctc tat aag aag atg atc gtc ttc			144
His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe			
35 40 45			
aag cca tac cag gcc tcc caa cat gac atg tgc cgc ttc cac tcc gag			192
Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu			
50 55 60			
gac tac att gac ttc ctg cag aga gtc agc ccc acc aat atg caa ggc			240
Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly			
65 70 75 80			
ttc acc aag agt ctt aat gcc ttc aac gta ggc gat gac tgc cca gtg			288
Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val			
85 90 95			
ttt ccc ggg ctc ttt gag ttc tgc tcg cgt tac aca ggc gca tct ctg			336
Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu			
100 105 110			
caa gga gca acc cag ctg aac aac aag atc tgt gat att gcc att aac			384
Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn			
115 120 125			
tgg gct ggt ggt ctg aag ctt gcc aag aag ttt gag gcc tct ggc ttc			432
Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys Phe Glu Ala Ser Gly Phe			
130 135 140			
tgc tat gtc aac gac att gtg att ggc atc ctg gag ctg ctc aag tac			480
Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr			
145 150 155 160			
cac cct cgg gtc tac att gac att gac atc cac cat ggt gac ggg			528
His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly			
165 170 175			
gtt caa gaa gct ttc tac ctc act gac cgg gtc atg acg gtc tcc ttc			576
Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe			
180 185 190			
cac aaa tac gga aat tac ttc ttc cct ggc aca ggt gac atg tat gaa			624
His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu			
195 200 205			
gtc ggg gca gag agt ggc cgc tac tac tgt ctg aac gtc ccc ctg cgg			672
Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg			
210 215 220			
gat ggc att gat gac cag agt tac aag cac ctt ttc cag ccg gtt atc			720
Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile			
225 230 235 240			

aac cag gta gtg gac ttc tac caa ccc acg tgc att gtg ctc cag tgt	768
Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys	
245 250 255	
gga gct gac tct ctg ggc tgt gat cga ttg ggc tgc ttt aac ctc agc	816
Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser	
260 265 270	
atc cga ggg cat ggg gaa tgc gtt gaa tat gtc aag agc ttc aat atc	864
Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile	
275 280 285	
cct cta ctc gtg ctg ggt ggt ggt tat act gtc cga aat gtt gcc	912
Pro Leu Leu Val Leu Gly Gly Gly Tyr Thr Val Arg Asn Val Ala	
290 295 300	
cgc tgc tgg aca tat gag aca tcg ctg ctg gta gaa gag gcc att agt	960
Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser	
305 310 315 320	
gag gag ctt ccc tat agt gaa tac ttc gag tac ttt gcc cca gac ttc	1008
Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe	
325 330 335	
aca ctt cat cca gat gtc agc acc cgc atc gag aat cag aac tca cgc	1056
Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg	
340 345 350	
cag tat ctg gac cag atc ctc cag aca atc ttt gaa aac ctg aag atg	1104
Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met	
355 360 365	
ctg aac cat gca cct agt gtc cag att cat gac gtg cct gca gac ctc	1152
Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu	
370 375 380	
ctg acc tat gac agg act gat gag gct gat gca gag gag agg ggt cct	1200
Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro	
385 390 395 400	
gag gag aac tat agc agg cca gag gca ccc aat gag ttc tat gat gga	1248
Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly	
405 410 415	
gac cat gac aat gac aag gaa agc gat gtg gag att taa	1287
Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile	
420 425	

<210> 18
 <211> 428
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Dominant negative mutant (H134K, H135L) of human histone deacetylase-3
 (HDAC3) gene

<400> 18
 Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe

1

5

10

15

His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
20 25 30

His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
35 40 45

Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
50 55 60

Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
65 70 75 80

Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
85 90 95

Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
100 105 110

Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
115 120 125

Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys Phe Glu Ala Ser Gly Phe
130 135 140

Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
145 150 155 160

His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
165 170 175

Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe
180 185 190

His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu
195 200 205

Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg
210 215 220

Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile
225 230 235 240

Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys
245 250 255

Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser
260 265 270

Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile
275 280 285

Pro Leu Leu Val Leu Gly Gly Gly Tyr Thr Val Arg Asn Val Ala
290 295 300

Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser
305 310 315 320

Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe
325 330 335

Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg
340 345 350

Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met
355 360 365

Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu
370 375 380

Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro
385 390 395 400

Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly
405 410 415

Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile
420 425

<210> 19
<211> 1287
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1287)
<223> Dominant negative mutant (H193L) of human histone deacetylase-3
(HDAC3)
gene

<400> 19
atg gcc aag acc gtg gcc tat ttc tac gac ccc gac gtg ggc aac ttc 48
Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe

1	5	10	15	
cac tac gga gct gga cac cct atg aag ccc cat cgc ctg gca ttg acc				96
His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr				
20	25	30		
cat agc ctg gtc ctg cat tac ggt ctc tat aag aag atg atc gtc ttc				144
His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe				
35	40	45		
aag cca tac cag gcc tcc caa cat gac atg tgc cgc ttc cac tcc gag				192
Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu				
50	55	60		
gac tac att gac ttc ctg cag aga gtc agc ccc acc aat atg caa ggc				240
Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly				
65	70	75	80	
ttc acc aag agt ctt aat gcc ttc aac gta ggc gat gac tgc cca gtg				288
Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val				
85	90	95		
ttt ccc ggg ctc ttt gag ttc tgc tcg cgt tac aca ggc gca tct ctg				336
Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu				
100	105	110		
caa gga gca acc cag ctg aac aac aag atc tgt gat att gcc att aac				384
Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn				
115	120	125		
tgg gct ggt ggt ctg cac cat gcc aag aag ttt gag gcc tct ggc ttc				432
Trp Ala Gly Gly Leu His Ala Lys Lys Phe Glu Ala Ser Gly Phe				
130	135	140		
tgc tat gtc aac gac att gtg att ggc atc ctg gag ctg ctc aag tac				480
Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr				
145	150	155	160	
cac cct cgg gtg ctc tac att gac att gac atc cac cat ggt gac ggg				528
His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly				
165	170	175		
gtt caa gaa gct ttc tac ctc act gac cgg gtc atg acg gtg tcc ttc				576
Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe				
180	185	190		
ctt aaa tac gga aat tac ttc ttc cct ggc aca ggt gac atg tat gaa				624
Leu Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu				
195	200	205		
gtc ggg gca gag agt ggc cgc tac tac tgt ctg aac gtg ccc ctg cgg				672
Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg				
210	215	220		
gat ggc att gat gac cag agt tac aag cac ctt ttc cag ccg gtt atc				720
Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile				
225	230	235	240	
aac cag gta gtg gac ttc tac caa ccc acg tgc att gtg ctc cag tgt				768
Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys				
245	250	255		

gga gct gac tct ctg ggc tgt gat cga ttg ggc tgc ttt aac ctc agc	816
Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser	
260 265 270	
atc cga ggg cat ggg gaa tgc gtt gaa tat gtc aag agc ttc aat atc	864
Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile	
275 280 285	
cct cta ctc gtg ctg ggt ggt ggt tat act gtc cga aat gtt gcc	912
Pro Leu Leu Val Leu Gly Gly Gly Tyr Thr Val Arg Asn Val Ala	
290 295 300	
cgc tgc tgg aca tat gag aca tcg ctg gta gaa gag gcc att agt	960
Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser	
305 310 315 320	
gag gag ctt ccc tat agt gaa tac ttc gag tac ttt gcc cca gac ttc	1008
Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe	
325 330 335	
aca ctt cat cca gat gtc agc acc cgc atc gag aat cag aac tca cgc	1056
Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg	
340 345 350	
cag tat ctg gac cag atc ctc cag aca atc ttt gaa aac ctg aag atg	1104
Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met	
355 360 365	
ctg aac cat gca cct agt gtc cag att cat gac gtg cct gca gac ctc	1152
Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu	
370 375 380	
ctg acc tat gac agg act gat gag gct gat gca gag gag agg ggt cct	1200
Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro	
385 390 395 400	
gag gag aac tat agc agg cca gag gca ccc aat gag ttc tat gat gga	1248
Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly	
405 410 415	
gac cat gac aat gac aag gaa agc gat gtg gag att taa	1287
Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile	
420 425	

<210> 20
 <211> 428
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Dominant negative mutant (H193L) of human histone deacetylase-3
 (HDAC3)
 gene

<400> 20
 Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
 1 5 10 15

His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
20 25 30

His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
35 40 45

Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
50 55 60

Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
65 70 75 80

Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
85 90 95

Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
100 105 110

Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
115 120 125

Trp Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe
130 135 140

Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
145 150 155 160

His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
165 170 175

Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe
180 185 190

Leu Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu
195 200 205

Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg
210 215 220

Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile
225 230 235 240

Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys
245 250 255

Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser

260

265

270

Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile
 275 280 285

Pro Leu Leu Val Leu Gly Gly Gly Tyr Thr Val Arg Asn Val Ala
 290 295 300

Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser
 305 310 315 320

Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe
 325 330 335

Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg
 340 345 350

Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met
 355 360 365

Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu
 370 375 380

Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro
 385 390 395 400

Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly
 405 410 415

Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile
 420 425

<210> 21
 <211> 1458
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1458)
 <223> human N-CoR (RD3) gene

<400> 21
 gaa gtc ctt cag cct gct cca cat caa gtg ata act aat ctc cct gaa 48
 Glu Val Leu Gln Pro Ala His Gln Val Ile Thr Asn Leu Pro Glu
 1 5 10 15

ggc gtt cgg ctt ccg aca act cga cca acc agg cca ccg ccc cct ctc 96
 Gly Val Arg Leu Pro Thr Thr Arg Pro Thr Arg Pro Pro Pro Pro Leu
 20 25 30

atc ccg tca tcc aaa acc aca gtg gct tca gaa aaa cca tct ttt ata Ile Pro Ser Ser Lys Thr Thr Val Ala Ser Glu Lys Pro Ser Phe Ile 35 40 45	144
atg gga ggc tcc atc tca cag gga aca cca ggc act tat ttg act tct Met Gly Gly Ser Ile Ser Gln Gly Thr Pro Gly Thr Tyr Leu Thr Ser 50 55 60	192
cat aat cag gct tcc tac act caa gaa aca ccc aag ccg tca gta gga His Asn Gln Ala Ser Tyr Thr Gln Glu Thr Pro Lys Pro Ser Val Gly 65 70 75 80	240
tct atc tct ctt gga ctg cca cgg caa cag gaa tct gcc aaa tca gct Ser Ile Ser Leu Gly Leu Pro Arg Gln Gln Glu Ser Ala Lys Ser Ala 85 90 95	288
act ttg ccc tac atc aag cag gaa gaa ttt tct ccc cga agc caa aac Thr Leu Pro Tyr Ile Lys Gln Glu Phe Ser Pro Arg Ser Gln Asn 100 105 110	336
tca caa cct gag ggt ctg ttg gtc agg gcc caa cat gaa ggt gta gtc Ser Gln Pro Glu Gly Leu Leu Val Arg Ala Gln His Glu Gly Val Val 115 120 125	384
aga ggt acc gca gga gcc ata caa gaa gga agt ata act cgg gga act Arg Gly Thr Ala Gly Ala Ile Gln Glu Gly Ser Ile Thr Arg Gly Thr 130 135 140	432
cca acc agc aaa att tca gtg gag agc att cca tcc cta cgg ggc tct Pro Thr Ser Lys Ile Ser Val Glu Ser Ile Pro Ser Leu Arg Gly Ser 145 150 155 160	480
atc act cag ggc acc ccg gct ctg ccc cag act ggc ata cca aca gag Ile Thr Gln Gly Thr Pro Ala Leu Pro Gln Thr Gly Ile Pro Thr Glu 165 170 175	528
gct ttg gtg aag ggg tcc att tcg aga atg ccc att gaa gac agc agt Ala Leu Val Lys Gly Ser Ile Ser Arg Met Pro Ile Glu Asp Ser Ser 180 185 190	576
cct gag aaa ggc aga gag gaa gct gca tcc aaa ggc cat gtt att tat Pro Glu Lys Gly Arg Glu Ala Ala Ser Lys Gly His Val Ile Tyr 195 200 205	624
gaa ggc aaa agt gga cat atc ttg tca tat gat aat att aag aat gcc Glu Gly Lys Ser Gly His Ile Leu Ser Tyr Asp Asn Ile Lys Asn Ala 210 215 220	672
cga gaa ggg act agg agt cca aga aca gct cat gaa atc agt tta aag Arg Glu Gly Thr Arg Ser Pro Arg Thr Ala His Glu Ile Ser Leu Lys 225 230 235 240	720
aga agc tat gaa tca gtg gaa gga aat ata aag caa ggg atg tca atg Arg Ser Tyr Glu Ser Val Glu Gly Asn Ile Lys Gln Gly Met Ser Met 245 250 255	768
agg gag tct cct gta tca gca ccg tta gag ggg ctg ata tgc cga gca Arg Glu Ser Pro Val Ser Ala Pro Leu Glu Gly Leu Ile Cys Arg Ala 260 265 270	816

tta ccc agg ggg agt cct cat tct gac ctc aaa gaa agg act gta ttg Leu Pro Arg Gly Ser Pro His Ser Asp Leu Lys Glu Arg Thr Val Leu 275 280 285	864
tct ggc tcc ata atg cag ggg aca cca aga gca aca act gaa agc ttt Ser Gly Ser Ile Met Gln Gly Thr Pro Arg Ala Thr Thr Glu Ser Phe 290 295 300	912
gaa gat ggc ctt aaa tat ccc aaa caa att aaa agg gaa agt cct ccc Glu Asp Gly Leu Lys Tyr Pro Lys Gln Ile Lys Arg Glu Ser Pro Pro 305 310 315 320	960
ata cga gca ttt gaa ggt gcc att acc aaa gga aaa cca tat gat ggc Ile Arg Ala Phe Glu Gly Ala Ile Thr Lys Gly Lys Pro Tyr Asp Gly 325 330 335	1008
atc acc acc atc aaa gaa atg ggg cgt tcc att cat gag att cca agg Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile Pro Arg 340 345 350	1056
caa gat att tta act cag gaa agt cgg aaa act cca gaa gtg gtc cag Gln Asp Ile Leu Thr Gln Glu Ser Arg Lys Thr Pro Glu Val Val Gln 355 360 365	1104
agc aca cgg ccg ata att gag ggt tcc att tcc cag ggc aca cca ata Ser Thr Arg Pro Ile Ile Glu Gly Ser Ile Ser Gln Gly Thr Pro Ile 370 375 380	1152
aag ttt gac aac aac tca ggt caa tct gcc atc aaa cac aat gtc aaa Lys Phe Asp Asn Asn Ser Gly Gln Ser Ala Ile Lys His Asn Val Lys 385 390 395 400	1200
tcc tta atc acg ggg cct agc aaa cta tcc cgt gga atg cct ccg ctg Ser Leu Ile Thr Gly Pro Ser Lys Leu Ser Arg Gly Met Pro Pro Leu 405 410 415	1248
gaa att gtg cca gag aac ata aaa gtg gta gaa cgg gga aaa tat gag Glu Ile Val Pro Glu Asn Ile Lys Val Val Glu Arg Gly Lys Tyr Glu 420 425 430	1296
gat gtg aaa gca ggc gag acc gtg cgt tcc cgg cac acg tca gtg gta Asp Val Lys Ala Gly Glu Thr Val Arg Ser Arg His Thr Ser Val Val 435 440 445	1344
agc tct ggc ccc tcc gtt ctt agg tcc aca ctg cat gaa gct ccc aaa Ser Ser Gly Pro Ser Val Leu Arg Ser Thr Leu His Glu Ala Pro Lys 450 455 460	1392
gca caa ctg agc cct ggg att tat gat gac acc agt gca cgg agg acc Ala Gln Leu Ser Pro Gly Ile Tyr Asp Asp Thr Ser Ala Arg Arg Thr 465 470 475 480	1440
cct gtg agt tat caa aac Pro Val Ser Tyr Gln Asn 485	1458

<210> 22
 <211> 486
 <212> PRT
 <213> Homo sapiens

<400> 22

Glu Val Leu Gln Pro Ala Pro His Gln Val Ile Thr Asn Leu Pro Glu
1 5 10 15

Gly Val Arg Leu Pro Thr Thr Arg Pro Thr Arg Pro Pro Pro Pro Leu
20 25 30

Ile Pro Ser Ser Lys Thr Thr Val Ala Ser Glu Lys Pro Ser Phe Ile
35 40 45

Met Gly Gly Ser Ile Ser Gln Gly Thr Pro Gly Thr Tyr Leu Thr Ser
50 55 60

His Asn Gln Ala Ser Tyr Thr Gln Glu Thr Pro Lys Pro Ser Val Gly
65 70 75 80

Ser Ile Ser Leu Gly Leu Pro Arg Gln Gln Glu Ser Ala Lys Ser Ala
85 90 95

Thr Leu Pro Tyr Ile Lys Gln Glu Glu Phe Ser Pro Arg Ser Gln Asn
100 105 110

Ser Gln Pro Glu Gly Leu Leu Val Arg Ala Gln His Glu Gly Val Val
115 120 125

Arg Gly Thr Ala Gly Ala Ile Gln Glu Gly Ser Ile Thr Arg Gly Thr
130 135 140

Pro Thr Ser Lys Ile Ser Val Glu Ser Ile Pro Ser Leu Arg Gly Ser
145 150 155 160

Ile Thr Gln Gly Thr Pro Ala Leu Pro Gln Thr Gly Ile Pro Thr Glu
165 170 175

Ala Leu Val Lys Gly Ser Ile Ser Arg Met Pro Ile Glu Asp Ser Ser
180 185 190

Pro Glu Lys Gly Arg Glu Glu Ala Ala Ser Lys Gly His Val Ile Tyr
195 200 205

Glu Gly Lys Ser Gly His Ile Leu Ser Tyr Asp Asn Ile Lys Asn Ala
210 215 220

Arg Glu Gly Thr Arg Ser Pro Arg Thr Ala His Glu Ile Ser Leu Lys
225 230 235 240

Arg Ser Tyr Glu Ser Val Glu Gly Asn Ile Lys Gln Gly Met Ser Met
245 250 255

Arg Glu Ser Pro Val Ser Ala Pro Leu Glu Gly Leu Ile Cys Arg Ala
260 265 270

Leu Pro Arg Gly Ser Pro His Ser Asp Leu Lys Glu Arg Thr Val Leu
275 280 285

Ser Gly Ser Ile Met Gln Gly Thr Pro Arg Ala Thr Thr Glu Ser Phe
290 295 300

Glu Asp Gly Leu Lys Tyr Pro Lys Gln Ile Lys Arg Glu Ser Pro Pro
305 310 315 320

Ile Arg Ala Phe Glu Gly Ala Ile Thr Lys Gly Lys Pro Tyr Asp Gly
325 330 335

Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile Pro Arg
340 345 350

Gln Asp Ile Leu Thr Gln Glu Ser Arg Lys Thr Pro Glu Val Val Gln
355 360 365

Ser Thr Arg Pro Ile Ile Glu Gly Ser Ile Ser Gln Gly Thr Pro Ile
370 375 380

Lys Phe Asp Asn Asn Ser Gly Gln Ser Ala Ile Lys His Asn Val Lys
385 390 395 400

Ser Leu Ile Thr Gly Pro Ser Lys Leu Ser Arg Gly Met Pro Pro Leu
405 410 415

Glu Ile Val Pro Glu Asn Ile Lys Val Val Glu Arg Gly Lys Tyr Glu
420 425 430

Asp Val Lys Ala Gly Glu Thr Val Arg Ser Arg His Thr Ser Val Val
435 440 445

Ser Ser Gly Pro Ser Val Leu Arg Ser Thr Leu His Glu Ala Pro Lys
450 455 460

Ala Gln Leu Ser Pro Gly Ile Tyr Asp Asp Thr Ser Ala Arg Arg Thr
465 470 475 480

Pro Val Ser Tyr Gln Asn
485

<210> 23
<211> 731
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(731)
<223> 5'-flanking region of Human interleukin-2 (IL-2) gene

<400> 23
ctgagtattt aacaatcgca ccctttaaaa aatgtacaat agacattaag agacttaaac 60
agatatataa tcattttaaa ttaaaatagc gttaaacagt acctcaagct caataagcat 120
tttaagtatt ctaatcttag tatttctcta gctgacatgt aagaagcaat ctatcttatt 180
gtatgcaatt agctcattgt gtggataaaa aggtaaaacc attctgaaac agggaaaccaa 240
tacacttcct gtttaatcaa caaatctaaa catttattct tttcatctgt ttactcttgc 300
tcttgtccac cacaatatgc tattcacatg ttcaagtgt tagtggaca aagaaaattt 360
tctgagttac ttttgtatcc ccacccctt aaagaaagga ggaaaaactg tttcatacag 420
aaggcgttaa ttgcatgaat tagagctatc acctaagtgt gggctaattgt aacaaagagg 480
gatttcacct acatccattc agtcagtctt tgggggtta aagaaattcc aaagagtcat 540
cagaagagga aaaatgaagg taatgtttt tcagacaggt aaagtctttg aaaatatgtg 600
taatatgtaa aacattttga caccccccata atattttcc agaattaaca gtataaattt 660
catctcttgt tcaagagttc cctatcactc tctttaatca ctactcacag taacctcaac 720
tcctgccaca a 731

<210> 24
<211> 527
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (73)..(506)
<223> 5'-flanking region of Human interleukin-2 (IL-2) gene

<220>
<221> misc_feature
<222> (4)..(9)
<223> a or g or c or t/u, unknown or other

<220>
<221> misc_feature
<222> (12)
<223> a or g or c or t/u, unknown or other

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<220>
<221> . misc_feature
<222> (56)
<223> a or g or c or t/u, unknown or other

<400> 24
gggnnnnnng gngatcctct accactata ggcgaattga atttagcggc cgcganttcg      60
cccttcgcta gctgctcttgc tccaccacaa tatgctattc acatgttcag tgtagtttta      120
ggacaaagaa aattttctga gttacttttgc tatccccacc cccttaaaga aaggaggaaa      180
aactgtttca tacagaaggc gttaattgca tgaatttagag ctatcaccta agtgtgggct      240
aatgttaacaa agagggattt cacctacatc cattcagtca gtctttgggg gttaaagaa      300
attccaaaga gtcatcagaa gagaaaaat gaaggtaatg tttttcaga caggtaaagt      360
cttgaaaat atgtgttaata tgtaaaacat tttgacaccc ccataatatt tttccagaat      420
taacagtata aattgcatct cttgttcaag agttccctat cactctctt aatcactact      480
cacagtaacc tcaactcctg ccacaagctt cgaagggcga attcggtt      527

<210> 25
<211> 900
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (57)..(875)
<223> Promoter region of Human GATA-1 gene

<400> 25
tgcctcttta ctatagggcg aattgaattt agcggccgca aattcgccct tgatctatcc      60
ctggctccca cctcagtttc cgcctccaa ggcagcatgg cgggcaagaa gttgaggcca      120
ctgtccctgg gtgttccatc ccccacaccc tcaccccaag acagcctgtt actgcggcgc      180
caacagccac ggtcgccatc atctgataag acttatctgc tgccccaggg cagggccggag      240
ctggcgtaag ccccagtggg gcgctaagtg agtgtgcccc tgcctccgc cagcactggc      300
ctggcctgca ggcttagcct gggcatcaa ggtatcccac aggctctagt tcaaatccag      360
cagaacctct ctgagcctca ctcttctcac ctgcaaaatg ggtacagcca catcccttct      420
ctccctgcag ccaggaagac gcacatacac aggagtctag cccacacccgg ccccgaccaa      480
attnaagggtt ttactctctg aaaagccca gtaagtcatg aaaccatatac tgctatttc      540
atttatcttg gtttcagcct attttgcttg tctggacact acagtccacg ggagcctagg      600
tcgagcgagg tccaagaatc cccagggtgg gcagggaggg tggaaagaggg cctccagtgc      660
ccaagaggtg ccccacaagc atgggacccg cccctcccc tggactgccc cacccactgg      720
ggcaccagcc actccctggg gaggagggag gagggagaag ggagggaggg agggagggag      780

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gaagggagcc tcaaaggcca aggccagcca ggacacccccc tgggatcaca ctgagcttgc 840
cacatccccca aggccggccga accctccgca accaccaaag cttataaggg cgaattcggt 900

<210> 26
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (11)..(647)
<223> Promoter region of Human GATA-1 gene

<400> 26
ttatggtacc accccagaag atgccaggag ggagttagcc agtcaggaa ggcttccgag 60
aagagaggac attgaagaag agtctcaaac ttaggcctga cggagaagac gcgcggccag 120
gacacccac ccccgccctc gtctccccc aagcctgatc tggcccccact gattccctta 180
tctgcccact cccagctgcc tccttgcgtgg ctgaactgtc gccgcagact tctgagcctg 240
cgccccctcc acggggatgg gggaggaaat ggggtgaggc ctggcctcac agcctcgaaa 300
tttccagctc ttgctggagg cagggctctg gggcgcccta ctcctcaccc ttggcttctc 360
ttcctgagcg ctctgtgctc tccagaaatg aagaaatggg gtgagtccag cggccaaacc 420
cttgtcttag ctcttagaca tgcctcgagc ctgcattcc ctgtgaggac agattccct 480
atgttgcac cgctgcttct aataataata atgatgatga taattccat ttacagagca 540
caccatttat ggtgtgccag cagggcctgt gctgagtggt tcctacccac gtggggggct 600
aggactttac ccgtttcca gatgaagaaa ctgaggctca gagggcgcta gcataagggc 660

<210> 27
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying the 5'-flanking region of Human interleukin-2
(IL-2) gene

<400> 27
tcgcttagcct gagtatttaa caatcgacc ct 32

<210> 28
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

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<223> PCR primer for amplifying the 5'-flanking region of Human interleukin-2
      (IL-2) gene

<400> 28
cgaagcttgt ggcaggagtt gaggttactg                                30

<210> 29
<211> 777
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(777)
<223> Corresponding to the sequence (+661 to +1437) in the GenBank database
      (Accession: HSIL05)

<400> 29
atcagtatcc ttgaatcgaa accttttct gagtatttaa caatcgacc cttaaaaaaaaa   60
tgtacataga cattaagaga cttaaacaga tatataatca ttttaaatta aaatagcgtt   120
aaacagtacc tcaagctcaa taagcattt aagtattcta atcttagtat ttctctagct   180
gacatgttaag aagcaatcta tcttattgta tgcaattagc tctttgtgtg gataaaaagg   240
taaaaaccatt ctgaaacagg aaaccaatac acttcctgtt taatcaacaa atctaaacat   300
ttattcttt catctgttta ctcttgctct tgtccaccac aatatgctat tcacatgttc   360
agtgttagttt tatgacaaag aaaattttct gagttacttt tgtatccccca cccctttaaa   420
gaaaggagga aaaactgttt catabagaag gcgttaattt catgaatttt agctatcacc   480
taagtgtggg ctaatgtaac aaagagggat ttcacctaca tccattcagt cagttttgg   540
gggtttaaag aaattccaaa gagtcatcag aagaggaaaa atgaaggtaa tgtttttca   600
gactggtaaa gtcttgaaa atatgtgtaa tatgtaaaac attttgacac cccataata   660
ttttccaga attaacagta taaattgcat ctcttgttca agagttccct atcactctt   720
aatcactact cacagtaacc tcaactcctg ccacaatgta caggatgcaa ctccgtt   777

<210> 30
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying the 5'-flanking region of Human interleukin-2
      (IL-2) gene

<400> 30
cgcttagctgc tcttgtccac cacaatatgc                                30

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<210> 31
<211> 538
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(538)
<223> Corresponding to the sequence (+901 to +1438) in the GenBank database
(Accession: HSIL05)

<400> 31
taaaaaccatt ctgaaacagg aaaccaatac acttcctgtt taatcaacaa atctaaacat      60
ttattctttt catctgttta ctcttgctct tgtccaccac aatatgctat tcacatgttc      120
agtgttagttt tatgacaaag aaaattttct gagttacttt tgtatccccca cccccttaaa      180
gaaaggagga aaaactgttt catacagaag gcgttaattt catgaatttag agctatcacc      240
taagtgtggg ctaatgtAAC aaagagggat ttcacctaca tccattcagt cagtcttgg      300
gggtttaaag aaattccaaa gagtcatcg aagaggaaaa atgaaggtaa tgtttttca      360
gactggtaaa gtcttgaaa atatgtgtaa tatgtaaaac attttgacac cccataata      420
tttttccaga attaacagta taaattgcat ctcttggtca agagttccct atcactctt      480
aatcactact cacagtaacc tcaactcctg ccacaatgta caggatgcaa ctcctgtc      538

<210> 32
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying the promoter region of Human GATA-1 gene

<400> 32
atagatctat ccctggctcc cacctcag                                28

<210> 33
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying the promoter region of Human GATA-1 gene

<400> 33
ataagctttg gtgggtgcgg agggttcg                                28

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

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<223> PCR primer for amplifying the promoter region of Human GATA-1 gene

<400> 34
atggtaccac cccagaagat gccaggag 28

<210> 35
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for amplifying the promoter region of Human GATA-1 gene

<400> 35
atgctagcgc cctctgagcc tcagttc 28

<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for amplifying a human histone deacetylase-1 (HDAC1) gene

<400> 36
gaggaattca agatggcgca gac 23

<210> 37
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for amplifying a human histone deacetylase-1 (HDAC1) gene

<400> 37
ggagcggccg cttcaggcca acttg 25

<210> 38
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for amplifying a human histone deacetylase-2 (HDAC2) gene

<400> 38
ggggatccat ggcgtacagt caag 24

<210> 39
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for amplifying a human histone deacetylase-2 (HDAC2) gene

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<400> 39
ggtcggccg ccaaattcag gggttgctg 29

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-3 (HDAC3) gene

<400> 40
ccggatccac catggccaag ac 22

<210> 41
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-3 (HDAC3) gene

<400> 41
gcagcggccg ccactcttaa atctccac 28

<210> 42
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-4 (HDAC4) gene

<400> 42
ggaaattcat gagctcccaa agccatcc 28

<210> 43
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-4 (HDAC4) gene

<400> 43
aaggcgccgc agcttcgagg gagtgctac 29

<210> 44
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-5 (HDAC5) gene

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```

<400> 44
ggcaagctta tgaactctcc caacgag 27

<210> 45
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-5 (HDAC5) gene

<400> 45
ggcgccgc gtcacagggc aggctcctg 29

<210> 46
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-6 (HDAC6) gene

<400> 46
gcgaagctta tgacctcaac cggccag 27

<210> 47
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-6 (HDAC6) gene

<400> 47
gcatgcggcc gcttagtgtg ggtggggcat atc 33

<210> 48
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-7 (HDAC7) gene

<400> 48
cgaattcagc cgcagcccat ggacct 26

<210> 49
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-7 (HDAC7) gene

```

```

<400> 49
cggtaccctg tgcacccgga tcacgg                                26

<210> 50
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-8 (HDAC8) gene

<400> 50
cgaattcttt aagcggaaaga tggagg                                26

<210> 51
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-8 (HDAC8) gene

<400> 51
aggtaaccgac cacatgcttc agattc                                26

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying a human histone deacetylase-3 (HDAC3) gene

<400> 52
ctgaattcac catggccaag accg                                24

<210> 53
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for adding a Flag sequence to a human histone deacetylase-3 (HDAC3) gene

<400> 53
gggcggccgc ctacttgtca tcgtcgtcct tgtaatcggt accaatctcc acatcgcttt      60
c                                         61

<210> 54
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

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<223> Flag sequence

<400> 54
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 55
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for adding a Kpn I site to a human histone deacetylase-1
(HDAC1) gene

<400> 55
atcggtaccg gccaacttga cctcctccctt g. 31

<210> 56
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for adding a Kpn I site to a human histone deacetylase-2
(HDAC2) gene

<400> 56
atcggtaccg gggttgctga gctgttctg 29

<210> 57
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for adding a Bgl II site to a human histone deacetylase-4
(HDAC4) gene

<400> 57
gatacatctc aggggcggct cctcttc 27

<210> 58
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence having a Flag nucleotide sequence

<400> 58
aattcctgca gagatctgat tacaaggacg acgatgacaa gtaggc 46

<210> 59
<211> 46
<212> DNA

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```

<213> Artificial Sequence

<220>
<223> Nucleotide sequence having a Flag nucleotide sequence

<400> 59
ggccgcctac ttgtcatcgt cgcccttgcatacagatctc tgcagg 46

<210> 60
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H802K, H803L) of
human histone deacetylase-4 (HDAC4) gene

<400> 60
cagtgacacc atatgaaacg agg 23

<210> 61
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H802K, H803L) of
human histone deacetylase-4 (HDAC4) gene

<400> 61
gcaagcttccaggggggcg 20

<210> 62
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H802K, H803L) of
human histone deacetylase-4 (HDAC4) gene

<400> 62
ccccctggaa agcttgcgga 20

<210> 63
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H802K, H803L) of
human histone deacetylase-4 (HDAC4) gene

```

```

<400> 63
gacatgtaca ggacgcgtagg gt 22

<210> 64
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H863L) of human
histone deacetylase-4 (HDAC4) gene

<400> 64
cctgtacatg tccctcccttc g 21

<210> 65
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H863L) of human
histone deacetylase-4 (HDAC4) gene

<400> 65
atacatcttag acaggggcgg 20

<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H140K, H141L) of
human
histone deacetylase-1 (HDAC1) gene

<400> 66
gaggaattca agatggcgca gac 23

<210> 67
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H140K, H141L) of
human
histone deacetylase-1 (HDAC1) gene

<400> 67
ctcggaatttc tttgcaagct tcagg 25

<210> 68
<211> 24
<212> DNA

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<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 68
gggcctgaag cttgcaaaga agtc

24

<210> 69

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 69
gtgaatatca atgtcaatgt acagc

25

<210> 70

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 70
gacggcgtgg aagaggcctt c

21

<210> 71

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 71
gaagtactct ccatacttaa gaaagg

26

<210> 72

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 72

ctgtgtcctt tcttaagtat ggagag

26

<210> 73
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 73
tctcggagcg ggttagttaac ag

22

<210> 74
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 74
aacccagctg aacaacaaga tctg

24

<210> 75
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 75
ctcaaacttc ttggcaagct tcagac

26

<210> 76
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 76
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25

<210> 77
<211> 21
<212> DNA

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<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H134K, H135L) of
human
histone deacetylase-3 (HDAC3) gene

<400> 77
cccgtcacca tggatgtt c

<210> 78
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H193L) of human
histone deacetylase-3 (HDAC3) gene

<400> 78
tgacatttgcacccatgtt gtg

<210> 79
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H193L) of human
histone deacetylase-3 (HDAC3) gene

<400> 79
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<210> 80
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H193L) of human
histone deacetylase-3 (HDAC3) gene

<400> 80
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<210> 81
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for creating a dominant negative mutant (H193L) of human
histone deacetylase-3 (HDAC3) gene

<400> 81
gagcacaatg cacgtgggtt gg

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<210> 82
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying RD3 sequence of human N-CoR gene

<400> 82
gggatccgtg aagtccottca gcctgctcc 29

<210> 83
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying RD3 sequence of human N-CoR gene

<400> 83
tgcggccgccc atgggtgagc ctctggaca 29

<210> 84
<211> 960
<212> DNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (1)..(960)
<223> Corresponding to the sequence (+5281 to +6240) in the GenBank database
(Acession: AF196971)

<400> 84
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catccctggc tcccacctca gtttccccgcc tccaaaggcag catggcgggc aagaagttga 120
ggccactgtc cctgggtgtt cctaccccca caccctcacc ccaagacagc ctgttactgc 180
ggcgccaaca gccacggtcg cctacatctg ataagactta tctgctgccc cagggcaggc 240
cgagactggc gtaagcccca gtggggcgct aagtgagtgt gcccctgcct cccgcccagca 300
ctggcctggc ctgcaggctt agcctgggtc atcaaggat cccacaggct ctatgtcaaa 360
tccagcagaa cctctctgag cctcactctt ctcacctgca aaatgggtac agccacatcc 420
cttctctccc tgcagccagg aagacgcaca tacacaggag tctagccac accggccccg 480
cacaattaa gggctttact ctctgaaaag cccagtgaag tcatgaaacc atatctgcta 540
ttttcattta tcttggtttc agcctatccc gcttgtctgg acactacagt ccacgggagc 600
ctaggtcgag cgaggtccaa gaatccccag ggtgggcagg gagggtgaa gagggcctcc 660
agtgcaccaag aggtgcacca caagcatggg acccgcccccc tccccctggac tgccccaccc 720

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actggggcac cagccactcc	ctggggagga gggaggagggg	agaaggaggagg gagggaggaga	780
gggaggaagg gagcctcaaa	ggccaaggcc agccaggaca	ccccctggga tcacactgag	840
cttgccacat ccccaaggcg	gccgaacctt ccgcaaccac	cagccaggt cagtctcagc	900
ccccagagag ccccccaccaa	ggcaaccctg ggcctgctgc	ccctaccctt atgcttgctc	960
<210> 85			
<211> 720			
<212> DNA			
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<220>			
<221> misc_feature			
<222> (1)..(720)			
<223> Corresponding to the sequence (+2321 to +3040) in the GenBank database			
(Accession: AF196971)			
<400> 85			
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gggagtgagc cagtcaggga aggcttccga	gaagagagga cattgaagaa	gagtctcaaa	120
cttaggcctg acggagaaga cgcgccgcca	ggacacccca ccccccgcct	cgtctcccc	180
aaagcctgat ctggcccccac tgattccctt	atctgcccac tcccagctgc	ctccttgctg	240
gctgaactgt cgccgcagac ttctgagcct	gcgccttc cacggggatg	ggggagggaa	300
tggggtgagg cctggcctca cagcctcggg	gtttccagct cttgctggag	gcagggctct	360
ggggcgcctt actcctcacc cttggcttct	cttcctgagc gctctgtgct	ctccagaaat	420
gaagaaatgg ggtgagtcca gcggccaaac	ccttgtctta gctcttagac	atgcctcgag	480
cctgccattc cctgtgagga cagattccc	tatgttgcga ccgctgcttc	taataataat	540
aatgatgatg ataattccca tttacagagc	acaccattta tggtgtgcca	gcagggccctg	600
tgctgagtgg ttcctaccca cgtggggggc	taggacttta cccgtttcc	agatgaagaa	660
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<210> 86			
<211> 12			
<212> DNA			
<213> homo sapiens			
<220>			
<221> misc_feature			
<222> (1)..(12)			
<223> Palindrome sequence founded on the 3' side of the GATA-E-box motif in			
promoter reagion of human GATA-1 gene			
<400> 86			
ctgtggccac ag			12